

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/090,867

DATE: 06/15/98  
TIME: 12:20:06

INPUT SET: S26648.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

1  
2  
3 (1) General Information:  
4  
5 (i) APPLICANT: Baumgartner, James W.  
6 Farrah, Theresa M.  
7 Foster, Donald C.  
8 Grant, Frank J.  
9 O'Hara, Patrick J.  
10  
11 (ii) TITLE OF INVENTION: Testis-Specific Receptor  
12  
13 (iii) NUMBER OF SEQUENCES: 33  
14  
15 (iv) CORRESPONDENCE ADDRESS:  
16 (A) ADDRESSEE: ZymoGenetics, Inc.  
17 (B) STREET: 1201 Eastlake Avenue East  
18 (C) CITY: Seattle  
19 (D) STATE: WA  
20 (E) COUNTRY: USA  
21 (F) ZIP: 98102  
22  
23 (v) COMPUTER READABLE FORM:  
24 (A) MEDIUM TYPE: Floppy disk  
25 (B) COMPUTER: IBM PC compatible  
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25  
28  
29 (vi) CURRENT APPLICATION DATA:  
30 (A) APPLICATION NUMBER:  
31 (B) FILING DATE:  
32 (C) CLASSIFICATION:  
33  
34 (viii) ATTORNEY/AGENT INFORMATION:  
35 (A) NAME: Parker, Gary E.  
36 (B) REGISTRATION NUMBER: 31,648  
37 (C) REFERENCE/DOCKET NUMBER: 95-33  
38  
39 (ix) TELECOMMUNICATION INFORMATION:  
40 (A) TELEPHONE: 206-442-6673  
41 (B) TELEFAX: 206-442-6678  
42  
43  
44 (2) INFORMATION FOR SEQ ID NO:1:  
45  
46 (i) SEQUENCE CHARACTERISTICS:

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/090,867

DATE: 06/15/98  
TIME: 12:20:07

INPUT SET: S26648.raw

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47      (A) LENGTH: 1289 base pairs
48      (B) TYPE: nucleic acid
49      (C) STRANDEDNESS: double
50      (D) TOPOLOGY: linear
51
52      (ii) MOLECULE TYPE: cDNA
53
54
55      (ix) FEATURE:
56          (A) NAME/KEY: CDS
57          (B) LOCATION: 49..1191
58
59
60      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
61
62      CCCCCGCCC GGGAGAGAGG CAATATCAAG GTTTTAAATC TCGGAGAA ATG GCT TTC      57
63                                         Met Ala Phe
64                                         1
65
66      GTT TGC TTG GCT ATC GGA TGC TTA TAT ACC TTT CTG ATA AGC ACA ACA      105
67      Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile Ser Thr Thr
68          5                      10                      15
69
70      TTT GGC TGT ACT TCA TCT TCA GAC ACC GAG ATA AAA GTT AAC CCT CCT      153
71      Phe Gly Cys Thr Ser Ser Ser Ser Asp Thr Glu Ile Lys Val Asn Pro Pro
72          20                      25                      30                      35
73
74      CAG GAT TTT GAG ATA GTG GAT CCC GGA TAC TTA GGT TAT CTC TAT TTG      201
75      Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Tyr Leu
76          40                      45                      50
77
78      CAA TGG CAA CCC CCA CTG TCT CTG GAT CAT TTT AAG GAA TGC ACA GTG      249
79      Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu Cys Thr Val
80          55                      60                      65
81
82      GAA TAT GAA CTA AAA TAC CGA AAC ATT GGT AGT GAA ACA TGG AAG ACC      297
83      Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr Trp Lys Thr
84          70                      75                      80
85
86      ATC ATT ACT AAG AAT CTA CAT TAC AAA GAT GGG TTT GAT CTT AAC AAG      345
87      Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys
88          85                      90                      95
89
90      GGC ATT GAA GCG AAG ATA CAC ACG CTT TTA CCA TGG CAA TGC ACA AAT      393
91      Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln Cys Thr Asn
92      100                      105                      110                      115
93
94      GGA TCA GAA GTT CAA AGT TCC TGG GCA GAA ACT ACT TAT TGG ATA TCA      441
95      Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr Trp Ile Ser
96          120                      125                      130
97
98      CCA CAA GGA ATT CCA GAA ACT AAA GTT CAG GAT ATG GAT TGC GTA TAT      489
99      Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp Cys Val Tyr

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**INPUT SET: S26648.raw**

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100																				
101																				
102	TAC	AAT	TGG	CAA	TAT	TTA	CTC	TGT	TCT	TGG	AAA	CCT	GGC	ATA	GGT	GTA		537		
103	Tyr	Asn	Trp	Gln	Tyr	Leu	Leu	Cys	Ser	Trp	Lys	Pro	Gly	Ile	Gly	Val				
104			150					155					160							
105																				
106	CTT	CTT	GAT	ACC	AAT	TAC	AAC	TTG	TTT	TAC	TGG	TAT	GAG	GGC	TTG	GAT		585		
107	Leu	Leu	Asp	Thr	Asn	Tyr	Asn	Leu	Phe	Tyr	Trp	Tyr	Glu	Gly	Leu	Asp				
108		165					170					175								
109																				
110	CAT	GCA	TTA	CAG	TGT	GTT	GAT	TAC	ATC	AAG	GCT	GAT	GGA	CAA	AAT	ATA		633		
111	His	Ala	Leu	Gln	Cys	Val	Asp	Tyr	Ile	Lys	Ala	Asp	Gly	Gln	Asn	Ile				
112	180					185					190					195				
113																				
114	GGA	TGC	AGA	TTT	CCC	TAT	TTG	GAG	GCA	TCA	GAC	TAT	AAA	GAT	TTC	TAT		681		
115	Gly	Cys	Arg	Phe	Pro	Tyr	Leu	Glu	Ala	Ser	Asp	Tyr	Lys	Asp	Phe	Tyr				
116					200					205					210					
117																				
118	ATT	TGT	GTT	AAT	GGA	TCA	TCA	GAG	AAC	AAG	CCT	ATC	AGA	TCC	AGT	TAT		729		
119	Ile	Cys	Val	Asn	Gly	Ser	Ser	Glu	Asn	Lys	Pro	Ile	Arg	Ser	Ser	Tyr				
120				215					220					225						
121																				
122	TTC	ACT	TTT	CAG	CTT	CAA	AAT	ATA	GTT	AAA	CCT	TTG	CCG	CCA	GTC	TAT		777		
123	Phe	Thr	Phe	Gln	Leu	Gln	Asn	Ile	Val	Lys	Pro	Leu	Pro	Pro	Val	Tyr				
124				230				235					240							
125																				
126	CTT	ACT	TTT	ACT	CGG	GAG	AGT	TCA	TGT	GAA	ATT	AAG	CTG	AAA	TGG	AGC		825		
127	Leu	Thr	Phe	Thr	Arg	Glu	Ser	Ser	Cys	Glu	Ile	Lys	Leu	Lys	Trp	Ser				
128		245					250					255								
129																				
130	ATA	CCT	TTG	GGA	CCT	ATT	CCA	GCA	AGG	TGT	TTT	GAT	TAT	GAA	ATT	GAG		873		
131	Ile	Pro	Leu	Gly	Pro	Ile	Pro	Ala	Arg	Cys	Phe	Asp	Tyr	Glu	Ile	Glu				
132	260					265					270					275				
133																				
134																				
135																				
136	ATC	AGA	GAA	GAT	GAT	ACT	ACC	TTG	GTG	ACT	GCT	ACA	GTT	GAA	AAT	GAA		921		
137	Ile	Arg	Glu	Asp	Asp	Thr	Thr	Leu	Val	Thr	Ala	Thr	Val	Glu	Asn	Glu				
138					280					285										

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153 Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu Ile Leu Val
154 340 345 350 355
155
156 ATA TTT GTA ACC GGT CTG CTT TTG CGT AAG CCA AAC ACC TAC CCA AAA 1161
157 Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr Tyr Pro Lys
158 360 365 370
159
160 ATG ATT CCA GAA TTT TTC TGT GAT ACA TGAAGACTTT CCATATCAAG 1208
161 Met Ile Pro Glu Phe Phe Cys Asp Thr
162 375 380
163
164 AGACATGGTA TTGACTCAAC AGTTTCCAGT CATGGCCAAA TGTTCATAT GAGTCTCAAT 1268
165
166 AAACCTGAATT TTTCTTGCGA A 1289
167
168
169 (2) INFORMATION FOR SEQ ID NO:2:
170
171 (i) SEQUENCE CHARACTERISTICS:
172 (A) LENGTH: 380 amino acids
173 (B) TYPE: amino acid
174 (D) TOPOLOGY: linear
175
176 (ii) MOLECULE TYPE: protein
177
178 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
179
180
181
182 Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile
183 1 5 10 15
184
185 Ser Thr Thr Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val
186 20 25 30
187
188 Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
189 35 40 45
190
191 Leu Tyr Leu Gln Trp Gln Pro Leu Ser Leu Asp His Phe Lys Glu
192 50 55 60
193
194 Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr
195 65 70 75 80
196
197 Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
198 85 90 95
199
200 Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln
201 100 105 110
202
203 Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr
204 115 120 125
205

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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/090,867

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206 Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp
207 130 135 140
208
209 Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly
210 145 150 155 160
211
212 Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu
213 165 170 175
214
215 Gly Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly
216 180 185 190
217
218 Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys
219 195 200 205
220
221 Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg
222 210 215 220
223
224 Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro
225 225 230 235 240
226
227 Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu
228 245 250 255
229
230 Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr
231 260 265 270
232
233 Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val
234 275 280 285
235
236 Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu
237 290 295 300
238
239 Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly
240 305 310 315 320
241
242 Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu
243 325 330 335
244
245 Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu
246 340 345 350
247
248 Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr
249 355 360 365
250
251 Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr
252 370 375 380
253
254

```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1167 base pairs

INPUT SET: S26648.raw

## \*\*\*\*\* PREVIOUSLY ERRORED SEQUENCES - EDITED \*\*\*\*\*

255 (2) INFORMATION FOR SEQ ID NO:3:

256

257 (i) SEQUENCE CHARACTERISTICS:

258 (A) LENGTH: 1167 base pairs

259 (B) TYPE: nucleic acid

260 (C) STRANDEDNESS: double

261 (D) TOPOLOGY: linear

262

263 (ii) MOLECULE TYPE: cDNA

264

265

266 (ix) FEATURE:

267 (A) NAME/KEY: CDS

268 (B) LOCATION: 10..1152

269

270

271 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

272

273 GATCCGCCC ATG GCT TTC GTT TGC TTG GCT ATC GGA TGC TTA TAT ACC 48

274 Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr

275 1 5 10

276

277 TTT CTG ATA AGC ACA ACA TTT GGC TGT ACT TCA TCT TCA GAC ACC GAG 96

278 Phe Leu Ile Ser Thr Thr Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu

279 15 20 25

280

281 ATA AAA GTT AAC CCT CCT CAG GAT TTT GAG ATA GTG GAT CCC GGA TAC 144

282 Ile Lys Val Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr

283 30 35 40 45

284

285 TTA GGT TAT CTC TAT TTG CAA TGG CAA CCC CCA CTG TCT CTG GAT CAT 192

286 Leu Gly Tyr Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His

287 50 55 60

288

289 TTT AAG GAA TAC ACA GTG GAA TAT GAA CTA AAA TAC CGA AAC ATT GGT 240

290 Phe Lys Glu Tyr Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly

291 65 70 75

292

293 AGT GAA ACA TGG AAG ACC ATC ATT ACT AAG AAT CTA CAT TAC AAA GAT 288

294 Ser Glu Thr Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp

295 80 85 90

296

297 GGG TTT GAT CTT AAC AAG GGC ATT GAA GCG AAG ATA CAC ACG CTT TTA 336

298 Gly Phe Asp Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu

299 95 100 105

300

301 CCA TGG CAA TGC ACA AAT GGA TCA GAA GTT CAA AGT TCC TGG GCA GAA 384

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/090,867

DATE: 06/15/98  
TIME: 12:20:13

INPUT SET: S26648.raw

302	Pro Trp Gln Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu	
303	110 115 120 125	
304		
305	ACT ACT TAT TGG ATA TCA CCA CAA GGA ATT CCA GAA ACT AAA GTT CAG	432
306	Thr Thr Tyr Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln	
307	130 135 140	
308		
309	GAT ATG GAT TGC GTA TAT TAC AAT TGG CAA TAT TTA CTC TGT TCT TGG	480
310	Asp Met Asp Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp	
311	145 150 155	
312		
313	AAA CCT GGC ATA GGT GTA CTT CTT GAT ACC AAT TAC AAC TTG TTT TAC	528
314	Lys Pro Gly Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr	
315	160 165 170	
316		
317	TGG TAT GAG GGC TTG GAT CTT GCA TTA CAG TGT GTT GAT TAC ATC AAG	576
318	Trp Tyr Glu Gly Leu Asp Leu Ala Leu Gln Cys Val Asp Tyr Ile Lys	
319	175 180 185	
320		
321	GCT GAT GGA CAA AAT ATA GGA TGC AGA TTT CCC TAT TTG GAG GCA TCA	624
322	Ala Asp Gly Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser	
323	190 195 200 205	
324		
325	GAC TAT AAA GAT TTC TAT ATT TGT GTT AAT GGA TCA TCA GAG AAC AAG	672
326	Asp Tyr Lys Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys	
327	210 215 220	
328		
329	CCT ATC AGA TCC AGT TAT TTC ACT TTT CAG CTT CAA AAT ATA GTT AAA	720
330	Pro Ile Arg Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys	
331	225 230 235	
332		
333	CCT TTG CCG CCA GTC TAT CTT ACT TTT ACT CGG GAG AGT TCA TGT GAA	768
334	Pro Leu Pro Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu	
335	240 245 250	
336		
337	ATT AAG CTG AAA TGG GGC ATA CCT TTG GGA CCT ATT CCA GCA AGG TGT	816
338	Ile Lys Leu Lys Trp Gly Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys	
339	255 260 265	
340		
341	TTT GAT TAT GAA ATT GAG ATC AGA GAA GAT GAT ACT ACC TTG GTG ACT	864
342	Phe Asp Tyr Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr	
343	270 275 280 285	
344		
345	GCT ACA GTT GAA AAT GAA ACA TAC ACC TTG AAA ACA ACA AAT GAA ACC	912
346	Ala Thr Val Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr	
347	290 295 300	
348		
349	CGA CAA TTA TGC TTT GTA GTA AGA AGC AAA GTG AAT ATT TAT TGC TCA	960
350	Arg Gln Leu Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser	
351	305 310 315	
352		
353	GAT GAC GGA ATT TGG AGT GAG TGG AGT GAT AAA CAA TGC TGG GAA GGT	1008
354	Asp Asp Gly Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly	

**INPUT SET: S26648.raw**

355	320					325					330						
356																	
357	GAA	GAC	CTA	TCG	AAG	AAA	ACT	TTG	CTA	CGT	TTC	TGG	CTA	CCA	TTT	GGT	1056
358	Glu	Asp	Leu	Ser	Lys	Lys	Thr	Leu	Leu	Arg	Phe	Trp	Leu	Pro	Phe	Gly	
359	335				340				345								
360																	
361																	
362																	
363	TTC	ATC	TTA	ATA	TTA	GTT	ATA	TTT	GTA	ACC	GGT	CTG	CTT	TTG	CGT	AAG	1104
364	Phe	Ile	Leu	Ile	Leu	Val	Ile	Phe	Val	Thr	Gly	Leu	Leu	Leu	Arg	Lys	
365	350				355				360				365				
366																	
367	CCA	AAC	ACC	TAC	CCA	AAA	ATG	ATT	CCA	GAA	TTT	TTC	TGT	GAT	ACA	TGAAGACTTT	1159
368	Pro	Asn	Thr	Tyr	Pro	Lys	Met	Ile	Pro	Glu	Phe	Phe	Cys	Asp	Thr		
369					370				375				380				
370																	
371	CCTCTAGA																1167
372																	
373																	



PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/090,867**

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Original Text